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1645

## RAW SEQUENCE LISTING

DATE: 02/12/2002

PATENT APPLICATION: US/09/988,113

TIME: 12:13:15

Input Set : A:\PT0.VSK.txt

Output Set: N:\CRF3\02122002\I988113.raw

3 <110> APPLICANT: Pecker, Iris  
4 Vlodavsky, Israel  
5 Feinstein, Elena  
7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE  
ACTIVITY AND  
8 EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS  
10 <130> FILE REFERENCE: 01/22781  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/988,113  
C--> 12 <141> CURRENT FILING DATE: 2001-11-19  
12 <150> PRIOR APPLICATION NUMBER: US 09/776,874  
13 <151> PRIOR FILING DATE: 2001-02-06  
15 <150> PRIOR APPLICATION NUMBER: US09/258,892  
16 <151> PRIOR FILING DATE: 1999-03-01  
18 <150> PRIOR APPLICATION NUMBER: PCT/US98/17954  
19 <151> PRIOR FILING DATE: 1998-08-31  
21 <150> PRIOR APPLICATION NUMBER: US 09/109,386  
22 <151> PRIOR FILING DATE: 1998-07-02  
24 <150> PRIOR APPLICATION NUMBER: US 08/922,170  
25 <151> PRIOR FILING DATE: 1997-09-02  
27 <160> NUMBER OF SEQ ID NOS: 47  
29 <170> SOFTWARE: PatentIn version 3.1  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 27  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Artificial sequence  
36 <220> FEATURE:  
37 <223> OTHER INFORMATION: Synthetic oligonucleotide  
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43 <210> SEQ ID NO: 2  
44 <211> LENGTH: 24  
45 <212> TYPE: DNA  
46 <213> ORGANISM: Artificial sequence  
48 <220> FEATURE:  
49 <223> OTHER INFORMATION: Synthetic oligonucleotide  
51 <400> SEQUENCE: 2  
52 ~~atagtgatgc catgtaactg aatc~~ 24  
55 <210> SEQ ID NO: 3  
56 <211> LENGTH: 23

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67 <210> SEQ ID NO: 4  
68 <211> LENGTH: 22  
69 <212> TYPE: DNA  
70 <213> ORGANISM: Artificial sequence  
72 <220> FEATURE:  
73 <223> OTHER INFORMATION: Synthetic oligonucleotide  
75 <400> SEQUENCE: 4  
76 gcatcttagc cgtctttctt cg 22  
79 <210> SEQ ID NO: 5  
80 <211> LENGTH: 15  
81 <212> TYPE: DNA  
82 <213> ORGANISM: Artificial sequence  
84 <220> FEATURE:  
85 <223> OTHER INFORMATION: Synthetic oligonucleotide  
87 <400> SEQUENCE: 5  
88 tttttttttt ttttt 15  
91 <210> SEQ ID NO: 6  
92 <211> LENGTH: 23  
93 <212> TYPE: DNA  
94 <213> ORGANISM: Artificial sequence  
96 <220> FEATURE:  
97 <223> OTHER INFORMATION: Synthetic oligonucleotide  
99 <400> SEQUENCE: 6  
100 ttccgatccca agaaggaatc aac 23  
103 <210> SEQ ID NO: 7  
104 <211> LENGTH: 24  
105 <212> TYPE: DNA  
106 <213> ORGANISM: Artificial sequence  
108 <220> FEATURE:  
109 <223> OTHER INFORMATION: Synthetic oligonucleotide  
111 <400> SEQUENCE: 7  
112 gtagtgatgc catgtaactg aatc 24  
115 <210> SEQ ID NO: 8  
116 <211> LENGTH: 9  
117 <212> TYPE: PRT  
118 <213> ORGANISM: Artificial sequence  
119 <220> FEATURE:  
121 <223> OTHER INFORMATION: Peptide derived from tryptic digestion of human heparinase  
123 <400> SEQUENCE: 8  
125 Tyr Gly Pro Asp Val Gly Gln Pro Arg  
126 1 5  
129 <210> SEQ ID NO: 9  
130 <211> LENGTH: 1721  
131 <212> TYPE: DNA  
132 <213> ORGANISM: Homo sapiens  
134 <400> SEQUENCE: 9  
135 ctatgaacttt cgaactctccg ctgcgcaggca gctgacgggg ggaagcaacca ggtgagccca 60

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139 cgetgggtcc ccttccccct ggcccccctgc cccgacctgc gcaagcacag gacgtcgtgg 180
141 acctggactt cttcaccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca 240
143 ccattgacgc caacctggcc acggaccgc ggttccctcat cctcctgggt tctccaaagc 300
145 ttctgtacct ggccagaggc ttgtctctcg cgtacctgag gtttgggtggc accaagacag 360
147 acttccctaatt ttctgatccc aagaaggaat caacctttga agagagaagt tactggcaat 420
149 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tctgtatgtg gaggagaagt 480
151 tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaagt 540
153 tcaagaacag cactactca agaagctctg tagatgtgct atacactttt gcaactgtct 600
155 caggactgga cttgatcttt ggccataatg cgttattaag aacagcagat ttgcagtgga 660
157 acagttctaa tgctcagttg ctcttgact actgctcttc caaggggtat aacatttctt 720
159 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt 780
161 cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa 840
163 atgcaaaact ctatggtcct gatgttggtc agcctcgaag aaagaaggct aagatgctga 900
165 agagcttccct gaaggctggt ggagaagtga ttgattcagt tacatggcat cactactatt 960
167 tgaatggacg gactgctacc agggagatt ttctaaacct tgatgtattg gacattttta 1020
169 ctccatctgt gcaaaaagti tccagggtg ilgagagcac caggccctggc aagaaggctc 1080
171 ggtaggaga aacaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg 1140
173 cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg 1200
175 tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgac 1260
177 ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aagggtgtta 1320
179 tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca 1380
181 ctgacaatcc aagggtataaa gaaggagatt taactctgta tgccataaac ctccataacg 1440
183 tcaccaagta cttgcggtta cctatcctt ttctaaaca gcaagtggat aaataccttc 1500
185 taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaactc 1560
187 taaagatggt ggatgatcaa acctggccac ctttaatgga aaaacctctc cggccaggaa 1620
189 gttcactggg cttgccagct ttctcatata gttttttgt gataagaaat gccaaagttg 1680
191 ctgcttgcat ctgaaaataa aatatactag tcttgacact g 1721

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195 &lt;210&gt; SEQ ID NO: 10

196 &lt;211&gt; LENGTH: 543

197 &lt;212&gt; TYPE: PRT

198 &lt;213&gt; ORGANISM: Homo sapiens

200 &lt;400&gt; SEQUENCE: 10

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203 1 5 10 15
206 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
207 20 25 30
210 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
211 35 40 45
214 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
215 50 55 60
218 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
219 65 70 75 80
222 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
223 85 90 95
226 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
227 100 105 110
230 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
231 115 120 125

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235      130      135      140
238 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
239 145      150      155      160
242 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
243      165      170      175
246 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
247      180      185      190
250 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
251      195      200      205
254 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
255      210      215      220
258 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
259 225      230      235      240
262 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
263      245      250      255
266 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
267      260      265      270
270 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
271      275      280      285
274 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
275      290      295      300
278 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
279 305      310      315      320
282 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
283      325      330      335
286 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
287      340      345      350
290 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
291      355      360      365
294 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
295      370      375      380
298 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
299 385      390      395      400
302 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
303      405      410      415
306 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
307      420      425      430
310 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
311      435      440      445
314 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
315      450      455      460
318 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
319 465      470      475      480
322 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
323      485      490      495
326 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
327      500      505      510
330 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
331      515      520      525

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334 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
335      530                      535                      540
339 <210> SEQ ID NO: 11
340 <211> LENGTH: 1721
341 <212> TYPE: DNA
342 <213> ORGANISM: Homo sapiens
344 <220> FEATURE:
345 <221> NAME/KEY: CDS
346 <222> LOCATION: (63)..(1691)
347 <223> OTHER INFORMATION:
350 <400> SEQUENCE: 11
351 ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca      60
353 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg      107
354 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
355      1                      5                      10                      15
357 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga      155
358 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
359      20                      25                      30
361 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag      203
362 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
363      35                      40                      45
365 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc      251
366 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
367      50                      55                      60
369 aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag      299
370 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
371      65                      70                      75
373 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt      347
374 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
375 80                      85                      90                      95
377 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc      395
378 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
379      100                      105                      110
381 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc      443
382 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
383      115                      120                      125
385 aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa      491
386 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
387      130                      135                      140
389 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag      539
390 Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
391      145                      150                      155
393 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act      587
394 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
395 160                      165                      170                      175
397 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta      635
398 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
399      180                      185                      190
401 tta gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/988,113

DATE: 02/12/2002

TIME: 12:13:16

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02122002\I988113.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47